

## CLAIMS

What is claimed is:

1. A method of analyzing gene expressions comprising acts of:  
determining a first gene expression pattern for a first condition, wherein the first  
5 gene expression pattern comprises a gene expression;  
forming a first spatial-expression pattern by:  
selecting a chromosomal region having an exon; and  
associating the gene expression within the first gene expression pattern  
with its corresponding exon.  
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2. The method of claim 1, wherein:  
the act of forming the first spatial-expression pattern further comprises an act of  
creating a first spatial-expression pattern signal wherein the first spatial-expression  
pattern signal is a representation of the first spatial-expression pattern where a magnitude  
15 of the first spatial-expression pattern signal at any point is determined by an expression  
level of the corresponding exon.
3. The method of claim 2, wherein:  
the magnitude of the first spatial-expression pattern signal at points spanning the  
20 chromosomal region are a function of the expression level of an exon at corresponding  
positions in the chromosomal region.
4. The method of claim 2, further comprising an act of:  
identifying first regular spatial patterns in the first spatial-expression pattern  
25 signal.

5. The method of claim 4, wherein  
the act of identifying first regular spatial patterns in the first spatial-expression  
pattern signal is performed through the use of Fourier transform signal processing.

5 6. The method of claim 5, further comprising an act of:  
identifying a group of genes contributing to local maximum points of the  
generated Fourier transform spectrum.

7. The method of claim 4, wherein  
10 the act of identifying first regular spatial patterns in the first spatial-expression  
pattern signal is performed through the use of Wavelet transform signal processing.

8. The method of claim 7, further comprising an act of:  
identifying a group of genes contributing to local maximum points of the  
15 generated Wavelet transformed signal at different scales and positions.

9. The method of claim 4, wherein:  
the act of identifying first regular spatial patterns in the first spatial-expression  
pattern signal identifies a set of genes.

20 10. The method of claim 9, wherein:  
the act of identifying first regular spatial patterns in the first spatial-expression  
pattern signal identifies a set of genes which participate in a common biological process  
or function.

25 11. The method of claim 1, further comprising acts of:  
determining a second gene expression pattern for a second condition, wherein the  
second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern  
with its corresponding exon.

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12. The method of claim 11, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern  
signal;

identifying second regular spatial patterns in the second spatial-expression pattern  
10 signal; and  
comparing the first and second regular spatial patterns.

13. The method of claim 11, further comprising an act of:

repeating the steps of determining a gene expression pattern and forming a  
15 spatial-expression pattern signal for any number of gene expression patterns.

14. The method of claim 13, further comprising acts of:

comparing all formed spatial-expression pattern signals.

20 15. The method of claim 14, wherein:

the act of comparing all formed spatial-expression pattern signals involves  
clustering all formed spatial-expression pattern signals.

16. The method of claim 15, further comprising acts of:

25 identifying gene groups contributing to the differences in significant changes in  
the first and second regular spatial-expression pattern signals.

17. The method of claim 1, wherein the chromosomal region is an entire chromosome.

18. The method of claim 11, wherein:

5 the first spatial-expression pattern and the second-expression pattern are selected from different chromosomes.

19. The method of claim 11, wherein:

10 the first spatial-expression and the second-expression pattern are selected from different genomes.

20. An apparatus for analyzing gene expressions, the apparatus comprising a computer system including a processor, a memory coupled with the processor, an input coupled with the processor for receiving input data, and an output coupled with the processor  
15 for outputting data, wherein the computer system further comprises means, residing in its processor and memory, for:

determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

20 selecting a chromosomal region having an exon; and

associating the gene expression within the first gene expression pattern with its corresponding exon.

21. An apparatus as set forth in claim 20, wherein:

25 the means for forming the first spatial-expression pattern further comprises an means for creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a

magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

22. An apparatus as set forth in claim 21, wherein:

5           the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

23. An apparatus as set forth in claim 21, further comprising an means for:

10           identifying first regular spatial patterns in the first spatial-expression pattern signal.

24. An apparatus as set forth in claim 23, wherein

15           the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

25. An apparatus as set forth in claim 24, further comprising an means for:

20           identifying a group of genes contributing to local maximum points of the generated Fourier transform spectrum.

26. An apparatus as set forth in claim 23, wherein

25           the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

27. An apparatus as set forth in claim 26, further comprising an means for:

identifying a group of genes contributing to local maximum points of the generated Wavelet transformed signal at different scales and positions.

28. An apparatus as set forth in claim 23, wherein:

5           the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes.

29. An apparatus as set forth in claim 28, wherein:

10           the means for identifying first regular spatial patterns in the first spatial-expression pattern signal identifies a set of genes which participate in a common biological process or function.

30. An apparatus as set forth in claim 20, further comprising acts of:

15           determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and  
            forming a second spatial-expression pattern by:  
                selecting a chromosomal region having an exon; and  
                associating a gene expression within the second gene expression pattern with its corresponding exon.

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31. An apparatus as set forth in claim 30, further comprising acts of:

            identifying first regular spatial patterns in the first spatial-expression pattern signal;  
            identifying second regular spatial patterns in the second spatial-expression pattern signal; and  
25           comparing the first and second regular spatial patterns.

32. An apparatus as set forth in claim 31, further comprising an means for:

repeating the steps of determining a gene expression pattern and forming a spatial-expression pattern signal for any number of gene expression patterns.

33. An apparatus as set forth in claim 30, further comprising acts of:

5       comparing all formed spatial-expression pattern signals.

34. An apparatus as set forth in claim 33, wherein:

the means for comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

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35. An apparatus as set forth in claim 34 further comprising acts of:

identifying gene groups contributing to the differences in significant changes in the first and second regular spatial-expression pattern signals.

15   36. An apparatus as set forth in claim 20, wherein the chromosomal region is an entire chromosome.

37. An apparatus as set forth in claim 11, wherein:

20       the first spatial-expression pattern and the second-expression pattern are selected from different chromosomes.

38. An apparatus as set forth in claim 30, wherein:

the first spatial-expression and the second-expression pattern are selected from different genomes.

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39. A computer program product for analyzing gene expressions, the computer program product comprising means, encoded in a computer-readable medium for:

determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having an exon; and

5 associating the gene expression within the first gene expression pattern with its corresponding exon.

40. A computer program product as set forth in claim 39, wherein:

10 the means for forming the first spatial-expression pattern further comprises an means for creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

15 41. A computer program product as set forth in claim 40, wherein:

the magnitude of the first spatial-expression pattern signal at points spanning the chromosomal region are a function of the expression level of an exon at corresponding positions in the chromosomal region.

20 42. A computer program product as set forth in claim 40, further comprising an means for:

identifying first regular spatial patterns in the first spatial-expression pattern signal.

25 43. A computer program product as set forth in claim 42, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.



44. A computer program product as set forth in claim 43, further comprising an means  
for:

5 identifying a group of genes contributing to local maximum points of the  
generated Fourier transform spectrum.

45. A computer program product as set forth in claim 42, wherein

10 the means for identifying first regular spatial patterns in the first spatial-  
expression pattern signal is performed through the use of Wavelet transform signal  
processing.

46. A computer program product as set forth in claim 45, further comprising an means  
for:

15 identifying a group of genes contributing to local maximum points of the  
generated Wavelet transformed signal at different scales and positions.

47. A computer program product as set forth in claim 42, wherein:

20 the means for identifying first regular spatial patterns in the first spatial-  
expression pattern signal identifies a set of genes.

48. A computer program product as set forth in claim 47, wherein:

25 the means for identifying first regular spatial patterns in the first spatial-  
expression pattern signal identifies a set of genes which participate in a common  
biological process or function.

49. A computer program product as set forth in claim 39, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the  
second gene expression pattern comprises a gene expression; and

forming a second spatial-expression pattern by:

selecting a chromosomal region having an exon; and

associating a gene expression within the second gene expression pattern  
with its corresponding exon.

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50. A computer program product as set forth in claim 49, further comprising acts of:

identifying first regular spatial patterns in the first spatial-expression pattern  
signal;

10 identifying second regular spatial patterns in the second spatial-expression pattern  
signal; and  
comparing the first and second regular spatial patterns.

51. A computer program product as set forth in claim 50, further comprising an means  
for:

15 repeating the steps of determining a gene expression pattern and forming a  
spatial-expression pattern signal for any number of gene expression patterns.

52. A computer program product as set forth in claim 49, further comprising acts of:  
comparing all formed spatial-expression pattern signals.

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53. A computer program product as set forth in claim 52, wherein:

the means for comparing all formed spatial-expression pattern signals involves  
clustering all formed spatial-expression pattern signals.

25 54. A computer program product as set forth in claim 53, further comprising acts of:

identifying gene groups contributing to the differences in significant changes in  
the first and second regular spatial-expression pattern signals.

55. A computer program product as set forth in claim 1, wherein the chromosomal region is an entire chromosome.

56. A computer program product as set forth in claim 39, wherein:

5       the first spatial-expression pattern and the second-expression pattern are selected from different chromosomes.

57. A computer program product as set forth in claim 39, wherein:

10       the first spatial-expression and the second-expression pattern are selected from different genomes.

58. A method of analyzing gene expressions comprising acts of:

      determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

15       forming a first spatial-expression pattern by:

          selecting a chromosomal region having an exon;

          associating the gene expression within the first gene expression pattern with its corresponding exon; and

20       creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

59. The method of claim 58, further comprising an act of:

25       identifying first regular spatial patterns in the first spatial-expression pattern signal.

60. The method of claim 59, wherein

the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

61. The method of claim 59, wherein

5       the act of identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

62. The method of claim 58, further comprising acts of:

10       determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and  
      forming a second spatial-expression pattern by:  
          selecting a chromosomal region having an exon; and  
          associating a gene expression within the second gene expression pattern with its corresponding exon.

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63. The method of claim 62, further comprising acts of:

      identifying first regular spatial patterns in the first spatial-expression pattern signal;  
      identifying second regular spatial patterns in the second spatial-expression pattern signal; and  
20       comparing the first and second regular spatial patterns.

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64. The method of claim 62, further comprising acts of:

      comparing all formed spatial-expression pattern signals.

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65. The method of claim 64, wherein:

      the act of comparing all formed spatial-expression pattern signals involves clustering all formed spatial-expression pattern signals.

66. An apparatus for analyzing gene expressions, the apparatus comprising a computer system including a processor, a memory coupled with the processor, an input coupled with the processor for receiving input data, and an output coupled with the processor for outputting data, wherein the computer system further comprises means, residing in its processor and memory, for:

determining a first gene expression pattern for a first condition, wherein the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having an exon;

associating the gene expression within the first gene expression pattern with its corresponding exon; and

creating a first spatial-expression pattern signal wherein the first spatial-expression pattern signal is a representation of the first spatial-expression pattern where a magnitude of the first spatial-expression pattern signal at any point is determined by an expression level of the corresponding exon.

67. An apparatus as set forth in claim 66, further comprising an means for:

identifying first regular spatial patterns in the first spatial-expression pattern

signal.

68. An apparatus as set forth in claim 67, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Fourier transform signal processing.

69. An apparatus as set forth in claim 67, wherein

the means for identifying first regular spatial patterns in the first spatial-expression pattern signal is performed through the use of Wavelet transform signal processing.

- 5     70. An apparatus as set forth in claim 58, further comprising acts of:  
          determining a second gene expression pattern for a second condition, wherein the  
second gene expression pattern comprises a gene expression; and  
          forming a second spatial-expression pattern by:  
              selecting a chromosomal region having an exon; and  
10            associating a gene expression within the second gene expression pattern  
with its corresponding exon.

71. An apparatus as set forth in claim 62, further comprising acts of:  
          identifying first regular spatial patterns in the first spatial-expression pattern  
15    signal;  
          identifying second regular spatial patterns in the second spatial-expression pattern  
signal; and  
          comparing the first and second regular spatial patterns.

- 20    72. An apparatus as set forth in claim 6, further comprising acts of:  
          comparing all formed spatial-expression pattern signals.

73. An apparatus as set forth in claim 64, wherein:  
          the means for comparing all formed spatial-expression pattern signals involves  
25    clustering all formed spatial-expression pattern signals.

74. A computer program product for analyzing gene expressions, the computer program  
product comprising means, encoded in a computer-readable medium for:

determining a first gene expression pattern for a first condition, wherein  
the first gene expression pattern comprises a gene expression;

forming a first spatial-expression pattern by:

selecting a chromosomal region having an exon;

5 associating the gene expression within the first gene expression pattern  
with its corresponding exon; and

creating a first spatial-expression pattern signal wherein the first spatial-  
expression pattern signal is a representation of the first spatial-expression pattern  
where a magnitude of the first spatial-expression pattern signal at any point is  
10 determined by an expression level of the corresponding exon.

75. A computer program product as set forth in claim 74, further comprising an means  
for:

15 identifying first regular spatial patterns in the first spatial-expression pattern  
signal.

76. A computer program product as set forth in claim 75, wherein

the means for identifying first regular spatial patterns in the first spatial-  
expression pattern signal is performed through the use of Fourier transform signal  
20 processing.

77. A computer program product as set forth in claim 75, wherein

the means for identifying first regular spatial patterns in the first spatial-  
expression pattern signal is performed through the use of Wavelet transform signal  
25 processing.

78. A computer program product as set forth in claim 74, further comprising acts of:

determining a second gene expression pattern for a second condition, wherein the second gene expression pattern comprises a gene expression; and  
forming a second spatial-expression pattern by:

- selecting a chromosomal region having an exon; and
- 5 associating a gene expression within the second gene expression pattern with its corresponding exon.

79. A computer program product as set forth in claim 78, further comprising acts of:

- identifying first regular spatial patterns in the first spatial-expression pattern
- 10 signal;
- identifying second regular spatial patterns in the second spatial-expression pattern
- signal; and
- comparing the first and second regular spatial patterns.

80. A computer program product as set forth in claim 78, further comprising acts of:

- comparing all formed spatial-expression pattern signals.

81. A computer program product as set forth in claim 81, wherein:

- the means for comparing all formed spatial-expression pattern signals involves
- 20 clustering all formed spatial-expression pattern signals.